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PATENT

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

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In re Application of: Roggen et al

Confirmation No: 2466

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Serial No.: 09/733,485

Group Art Unit: 1645

Filed: December 8, 2000

Examiner: T. Bhatti

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For: High Throughput Screening (HTS) Assays

AMENDMENT AND RESPONSE TO NOTICE TO FILE MISSING PARTS  
AND TO NOTICE TO COMPLY WITH SEQUENCE REQUIREMENTS

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Sir:

In response to the Notice to Comply with Sequence Rules dated February 20, 2002, please amend the above-identified application as follows (a marked up version pursuant to 37 C.F.R. 1.21 is attached hereto):

IN THE SPECIFICATION:

2 Please replace the paragraph from page 41, line 15 – page 42, line 2 with:

B1  
In another embodiment, the library is designed, such that recognition sites for post-translational modifications are introduced in the epitope areas, and the library is expressed in a suitable host organism capable of the corresponding post-translational modification. These post-translational modifications may serve to shield the epitope and hence lower the immunogenicity of the protein variant relative to the protein backbone. Post-translational modifications include glycosylation, phosphorylation, N-terminal processing, acylation, ribosylation and sulfatation. A good example is N-glycosylation. N-glycosylation is found at sites of the sequence Asn-Xaa-Ser, Asn-Xaa-Thr, or Asn-Xaa-Cys, in which neither the Xaa residue nor the amino acid following the tri-peptide consensus sequence is a proline (T. E. Creighton, "Proteins – Structures and Molecular Properties", 2nd edition, W.H. Freeman and Co., New York, 1993, pp. 91-93). It is thus desirable to introduce such recognition sites in the sequence of the backbone protein. The specific nature of the glycosyl chain of the glycosylated protein variant may be linear or branched depending on the protein and the host cells. Another example is phosphorylation: The protein sequence can be